SEQUENCE LISTING

<110> Schall, Thomas J.
Penfold, Mark E.T.
ChemoCentryx, Inc.

#16

<120> Inhibition of CMV Infection and Dissemination

<130> 019934-002510US

<140> US 09/944,049
<141> 2001-08-30

<150> US 60/229,365
<151> 2000-08-30

<160> 48

<170> PatentIn Ver. 2.1

<210> 1
<211> 1065
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) Toledo strain open reading frame US28 (AU4.1)

<220>
<221> CDS
<222> (1)..(1065)
<223> HCMV Toledo US28

<400> 1
atgacaccga cgacgacgac cgcggaactc acgacggagt ttgactacga tgaagccgcg 60
actccttgtg ttttcaccga cgtgcttaat cagtcaaagc cggttacgtt gtttctgtac 120
ggcgttgtct ttctgttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
cgacgtcgga ttcaatgctc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atatcggcct 420
gtaaaacagg cctgcctttt cagtattttt tggtggatct ttgccgtgat catcgccatt 480
ccacatttta tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
gaggtcagct acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
ctcagtgtca tcagctactg ctactaccgc atttccagaa tcgttgcggt gtctcagtcg 660
cgccacaaag gtcgcattgt acgggtactt atagcggtcg tgcttgtctt tatcatcttt 720
tggctgccgt accacctaac gctgtttgtg gacacgttaa aactcctcaa atggatctcc 780
agcagctgcg agttcgaaag atcgctcaaa cgtgcgctca tcttgaccga gtcgctcgcc 840
ttttgtcact gttgtctcaa tccgctgctg tacgtcttcg tgggcaccaa gtttcggcaa 900
gaactgcact gtctgctggc cgagtttcgc cagcgactct tttcccgcga tgtatcctgg 960
taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac atcttccgac 1020
acgctgtccg acgaggtgtg tcgcgtctca caaattatac cgtaa 1065

<210> 2
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) Toledo strain open reading frame US28 (AU4.1)

<400> 2

```
Met Thr Pro Thr Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
  1               5                  10                  15

Asp Glu Ala Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
             20                  25                  30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
         35                  40                  45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
     50                  55                  60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
 65                  70                  75                  80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
                 85                  90                  95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
            100                 105                 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
        115                 120                 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
    130                 135                 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
145                 150                 155                 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
                165                 170                 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
            180                 185                 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
        195                 200                 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
    210                 215                 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
225                 230                 235                 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
                245                 250                 255

Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
            260                 265                 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
        275                 280                 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
    290                 295                 300
```

```
Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
305                 310                 315                 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
                325                 330                 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
            340                 345                 350

Ile Pro
```

<210> 3
<211> 1065
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) VHL/E strain open reading frame US28

<220>
<221> CDS
<222> (1)..(1065)
<223> HCMV VHL/E US28

<400> 3
atgacaccga cgacgacgac cgcggaactc acgacggagt ttgactacga cgatgaagcg 60
actccctgtg tcctcaccga cgtgcttaat cagtcgaagc cagtcacgtt gtttctgtac 120
ggcgttgtct ttctcttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
cgacgtcgga ttcaatgttc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atatcggcct 420
gtaaaacagg cctgcctttt cagtattttt tggtggatct ttgccgtgat catcgccatt 480
ccacacttta tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
gaggtcagtt acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
ctcagtgtca tcagctactg ctactaccgc atttccagaa tcgttgcggt gtctcagtcg 660
cgccacaaag gccgcattgt acgggtactt atagcggtcg tgcttgtctt tatcatcttt 720
tggctgccgt accacctgac gctgtttgtg gacacgttga aactgctcaa atggatctcc 780
agcagctgcg agttcgaaaa atcactcaag cgcgcgctca tcttgaccga gtcactcgcc 840
ttttgtcact gttgtctcaa tccgctgctg tacgtcttcg tgggcaccaa gtttcggcaa 900
gaactgcact gtctgctggc cgagtttcgc cagcgactgt tttcccgcga tgtatcctgg 960
taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac gtcttccgac 1020
acgctgtccg acgaggcgtg tcgcgtctca caaattatac cgtaa 1065

<210> 4
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) VHL/E strain open reading frame US28

<400> 4
```
Met Thr Pro Thr Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
  1               5                  10                  15
```

```
Asp Asp Glu Ala Thr Pro Cys Val Leu Thr Asp Val Leu Asn Gln Ser
            20                  25                  30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
        35                  40                  45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
    50                  55                  60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
65                  70                  75                  80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
                85                  90                  95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
            100                 105                 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
        115                 120                 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
    130                 135                 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
145                 150                 155                 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
                165                 170                 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
            180                 185                 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
        195                 200                 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
    210                 215                 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
225                 230                 235                 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
                245                 250                 255

Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Lys Ser Leu Lys Arg Ala
            260                 265                 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
        275                 280                 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
    290                 295                 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
305                 310                 315                 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
                325                 330                 335
```

Thr Ser Ser Asp Thr Leu Ser Asp Glu Ala Cys Arg Val Ser Gln Ile
340 345 350

Ile Pro

<210> 5
<211> 1020
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.1

<220>
<221> CDS
<222> (1)..(1020)
<223> rhUS28.1

<400> 5
atgaataaca catcttgcaa cttcaacgtc actctcaacg catcggcacc aagccgatac 60
atagctattg ctatgtacag cattgttatc tgtatcgggt tggttggaaa cctgctgtta 120
tgcatcgtgt tagtcaagaa acgcaaactg cgatattcca gcgatgttta ttttttccac 180
gcctctatgg ccgacctcgt cagcactgtc atgctaccgc tctggctaca ttatgtcctc 240
aactttgccc aactctctcg aggagcctgt atcagctttt cggtgacttt ctatgttccc 300
cttttcgttc aggcctggtt actcatttcc atcgctatgg agcgatattc caacttagta 360
tggatggcac ccattagcgt taagacggcc tttaaacact gcataggaac ctggatcgta 420
tctgccttcg tggcatcacc ctactacgca tacagaaact cacacgacga acacgaatgc 480
attctaggaa actacacttg gcacattaac gaaccgctac acacgtgtat ggatgtggtg 540
atcatagtat ggacctttt ggccccagta ctggtaacca ttatagcaag cgtcaaaatg 600
agacgaacga cctggggcaa tactaggtta aacgaaaaga acagcgacat tcttatagta 660
ctagttgtca tgacagtgtt cttttgggga ccgtttaata tcgtgttggt tattgacaat 720
attttacaga gatactatga taccacgaat tgcgatgtag aaaagattaa acatatcatg 780
gctatgatct cagaagccat tgtttatttt cgcggtatta cagcacctat tatttatgta 840
gggattagtg gcagatttcg cgaagagatt tactctctgt ttagacgcca gccgtataac 900
gatttggacc ccgatgccaa tcaattcatg attgaactca ctagccaggg aagaagtaga 960
aatagaaatg ctagacaatc ggaaagcaat gtaccgcaac cagaagaatg cttctggtaa 1020

<210> 6
<211> 339
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.1

<400> 6
Met Asn Asn Thr Ser Cys Asn Phe Asn Val Thr Leu Asn Ala Ser Ala
1 5 10 15

Pro Ser Arg Tyr Ile Ala Ile Ala Met Tyr Ser Ile Val Ile Cys Ile
20 25 30

Gly Leu Val Gly Asn Leu Leu Leu Cys Ile Val Leu Val Lys Lys Arg
35 40 45

Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
50 55 60

```
Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
 65                  70                  75                  80

Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
                85                  90                  95

Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
            100                 105                 110

Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
        115                 120                 125

Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
    130                 135                 140

Ala Ser Pro Tyr Tyr Ala Tyr Arg Asn Ser His Asp Glu His Glu Cys
145                 150                 155                 160

Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
                165                 170                 175

Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
            180                 185                 190

Thr Ile Ile Ala Ser Val Lys Met Arg Arg Thr Thr Trp Gly Asn Thr
        195                 200                 205

Arg Leu Asn Glu Lys Asn Ser Asp Ile Leu Ile Val Leu Val Val Met
    210                 215                 220

Thr Val Phe Phe Trp Gly Pro Phe Asn Ile Val Leu Val Ile Asp Asn
225                 230                 235                 240

Ile Leu Gln Arg Tyr Tyr Asp Thr Thr Asn Cys Asp Val Glu Lys Ile
                245                 250                 255

Lys His Ile Met Ala Met Ile Ser Glu Ala Ile Val Tyr Phe Arg Gly
            260                 265                 270

Ile Thr Ala Pro Ile Ile Tyr Val Gly Ile Ser Gly Arg Phe Arg Glu
        275                 280                 285

Glu Ile Tyr Ser Leu Phe Arg Arg Gln Pro Tyr Asn Asp Leu Asp Pro
    290                 295                 300

Asp Ala Asn Gln Phe Met Ile Glu Leu Thr Ser Gln Gly Arg Ser Arg
305                 310                 315                 320

Asn Arg Asn Ala Arg Gln Ser Glu Ser Asn Val Pro Gln Pro Glu Glu
                325                 330                 335

Cys Phe Trp
```

<210> 7
<211> 1002
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.2

<220>
<221> CDS
<222> (1)..(1002)
<223> rhUS28.2

<400> 7
atgaccaacg ccggacactg tcacataaac gaaagtctcg cgtcgtatgg aatcgctccc 60
gcagctacca ttaccttata cagcattgcg ggaatctgcg gtgtcacggg aaatctgtta 120
atacttttgg ttttgttcac gagacgcata cactggttcg caaatgacat ctactatctc 180
aacatgatct ttacagactt tcttgttttc attacattac ccgcctgggt ttactacctg 240
ctgaattaca cacaactctc acactatgcc tgcattgctc tatcatttgt tttttacgtt 300
tccattttta ttcaagctga ctttatggta gcagtggcta tcgagcgtta tcgaagccta 360
gtgaaaaaca aacccccttag cgtaaaaaaa gccagcgtca gctgcgcgtg catctggatc 420
attgttatta tagtgtcttc accatactac atgtttagat cgcaacacga aacaaattct 480
tgcattctag gaaactacac ctggcatatg aacagtcctt ttcgcaccac aatggacgca 540
tccattaaca tttggtcttt tgtcgttccg gccgtgacga ccttgttaat agccagacga 600
atttatgtat gtacttcagg caacaaaaaa atgaacgcca gagccagtgg tttgttagag 660
gccatggtga ttagcatgtt attcttcgga ggacttttca acctgaacat ctttcgagac 720
atagtttcgg acacatcgga agacaataaa gactgcacat atcttaagca ggaacacttt 780
attcgcatgg tcggtgtggc cctcgtttac gggcgcgcta tattcaaccc ttttatgtat 840
atgtgtgtga gtaccagatt gcgccaagaa ataaaatgtt tgtttatgcg aataccttat 900
gaaacactag atgcagaaca cgctaaactc atggttaatt taaaaaacag aaatgctaat 960
gtacccgatc ctaaacctcg tgaatatgaa tctgtgttat ag 1002

<210> 8
<211> 333
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.2

<400> 8
Met Thr Asn Ala Gly His Cys His Ile Asn Glu Ser Leu Ala Ser Tyr
1 5 10 15

Gly Ile Ala Pro Ala Ala Thr Ile Thr Leu Tyr Ser Ile Ala Gly Ile
20 25 30

Cys Gly Val Thr Gly Asn Leu Leu Ile Leu Leu Val Leu Phe Thr Arg
35 40 45

Arg Ile His Trp Phe Ala Asn Asp Ile Tyr Tyr Leu Asn Met Ile Phe
50 55 60

Thr Asp Phe Leu Val Phe Ile Thr Leu Pro Ala Trp Val Tyr Tyr Leu
65 70 75 80

Leu Asn Tyr Thr Gln Leu Ser His Tyr Ala Cys Ile Ala Leu Ser Phe
85 90 95

Val Phe Tyr Val Ser Ile Phe Ile Gln Ala Asp Phe Met Val Ala Val
100 105 110

```
Ala Ile Glu Arg Tyr Arg Ser Leu Val Lys Asn Lys Pro Leu Ser Val
        115                 120                 125

Lys Lys Ala Ser Val Ser Cys Ala Cys Ile Trp Ile Ile Val Ile Ile
    130                 135                 140

Val Ser Ser Pro Tyr Tyr Met Phe Arg Ser Gln His Glu Thr Asn Ser
145                 150                 155                 160

Cys Ile Leu Gly Asn Tyr Thr Trp His Met Asn Ser Pro Phe Arg Thr
                165                 170                 175

Thr Met Asp Ala Ser Ile Asn Ile Trp Ser Phe Val Val Pro Ala Val
            180                 185                 190

Thr Thr Leu Leu Ile Ala Arg Arg Ile Tyr Val Cys Thr Ser Gly Asn
        195                 200                 205

Lys Lys Met Asn Ala Arg Ala Ser Gly Leu Leu Glu Ala Met Val Ile
    210                 215                 220

Ser Met Leu Phe Phe Gly Gly Leu Phe Asn Leu Asn Ile Phe Arg Asp
225                 230                 235                 240

Ile Val Ser Asp Thr Ser Glu Asp Asn Lys Asp Cys Thr Tyr Leu Lys
                245                 250                 255

Gln Glu His Phe Ile Arg Met Val Gly Val Ala Leu Val Tyr Gly Arg
            260                 265                 270

Ala Ile Phe Asn Pro Phe Met Tyr Met Cys Val Ser Thr Arg Leu Arg
        275                 280                 285

Gln Glu Ile Lys Cys Leu Phe Met Arg Ile Pro Tyr Glu Thr Leu Asp
    290                 295                 300

Ala Glu His Ala Lys Leu Met Val Asn Leu Lys Asn Arg Asn Ala Asn
305                 310                 315                 320

Val Pro Asp Pro Lys Pro Arg Glu Tyr Glu Ser Val Leu
                325                 330
```

<210> 9
<211> 1014
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.3

<220>
<221> CDS
<222> (1)..(1014)
<223> rhUS28.3

<400> 9
atgaccaaca ctaacaatac gacttgtcat ctcaacggaa ctttcgaaac ttttaaaatc 60
acccgtccag tagccatcag cgcctacact gtactcgtgg ttatcggact tttgggaaac 120
attgtgctgc tcagcgtgct cgtcgtgaaa cgcaagctca agtttccgaa tgacatttac 180

```
tttttcaacg cgtctttggc agacgttttt gccgtctgca tgttgcccgc ctgggttaac 240
tatgcactgg actccacaca acttagcaag ttctcatgta tcacttttac gtttggtttt 300
tacgtctccc tgttcatcca ggcctggatg ctcattctgg tcaccctgga gcgatacgga 360
tctctagtct ggatcgcccc gatcaccaga aacaaagcca tagcgaattg tgtactcttt 420
tggcttgttt ccatcttctt ggccgcacct tactactctt ttagaaacga aagcaacgaa 480
caccaatgca tcatgagaaa ctatacctgg agcgttggtg aaacatggca catagccctg 540
gatttcttaa ttacgctcat tacatttatc atgccagtga ctattgtgtt agctctgagt 600
ttcaaaatgg ccagatggtc aacctttggt tacagaaacc tcaccagcag aaccagtctt 660
atccttattt tgatactgac agtagcagca gggttctggg gacctttca cctatttatg 720
tttatagaaa acgtggcagg gcagatttac cacattcaaa aggattgctg gtacttacag 780
ctcagacact tgtgtagctt gatgaccgaa accctagtgt ttctacgttc agtttttaac 840
ccttatattt atatgataat cagttacaag tttaggcagc aggtgcgcag tctactcaag 900
cgtactcagt atgatgcttt ggacacgact cagttagcag aaactatgca gctgaaagcg 960
aaaggtgtgc cggtgtccga ccccgcgccg catgactgcg aatgcttttt gtaa       1014
```

<210> 10
<211> 337
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.3

<400> 10

```
Met Thr Asn Thr Asn Asn Thr Thr Cys His Leu Asn Gly Thr Phe Glu
  1               5                  10                  15

Thr Phe Lys Ile Thr Arg Pro Val Ala Ile Ser Ala Tyr Thr Val Leu
             20                  25                  30

Val Val Ile Gly Leu Leu Gly Asn Ile Val Leu Leu Ser Val Leu Val
         35                  40                  45

Val Lys Arg Lys Leu Lys Phe Pro Asn Asp Ile Tyr Phe Phe Asn Ala
     50                  55                  60

Ser Leu Ala Asp Val Phe Ala Val Cys Met Leu Pro Ala Trp Val Asn
 65                  70                  75                  80

Tyr Ala Leu Asp Ser Thr Gln Leu Ser Lys Phe Ser Cys Ile Thr Phe
                 85                  90                  95

Thr Phe Gly Phe Tyr Val Ser Leu Phe Ile Gln Ala Trp Met Leu Ile
            100                 105                 110

Leu Val Thr Leu Glu Arg Tyr Gly Ser Leu Val Trp Ile Ala Pro Ile
        115                 120                 125

Thr Arg Asn Lys Ala Ile Ala Asn Cys Val Leu Phe Trp Leu Val Ser
    130                 135                 140

Ile Phe Leu Ala Ala Pro Tyr Tyr Ser Phe Arg Asn Glu Ser Asn Glu
145                 150                 155                 160

His Gln Cys Ile Met Arg Asn Tyr Thr Trp Ser Val Gly Glu Thr Trp
                165                 170                 175

His Ile Ala Leu Asp Phe Leu Ile Thr Leu Ile Thr Phe Ile Met Pro
            180                 185                 190
```

Val Thr Ile Val Leu Ala Leu Ser Phe Lys Met Ala Arg Trp Ser Thr
195 200 205

Phe Gly Tyr Arg Asn Leu Thr Ser Arg Thr Ser Leu Ile Leu Ile Leu
210 215 220

Ile Leu Thr Val Ala Ala Gly Phe Trp Gly Pro Phe His Leu Phe Met
225 230 235 240

Phe Ile Glu Asn Val Ala Gly Gln Ile Tyr His Ile Gln Lys Asp Cys
245 250 255

Trp Tyr Leu Gln Leu Arg His Leu Cys Ser Leu Met Thr Glu Thr Leu
260 265 270

Val Phe Leu Arg Ser Val Phe Asn Pro Tyr Ile Tyr Met Ile Ile Ser
275 280 285

Tyr Lys Phe Arg Gln Gln Val Arg Ser Leu Leu Lys Arg Thr Gln Tyr
290 295 300

Asp Ala Leu Asp Thr Thr Gln Leu Ala Glu Thr Met Gln Leu Lys Ala
305 310 315 320

Lys Gly Val Pro Val Ser Asp Pro Ala Pro His Asp Cys Glu Cys Phe
325 330 335

Leu

<210> 11
<211> 987
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.4

<220>
<221> CDS
<222> (1)..(987)
<223> rhUS28.4

<400> 11
atgaattcga gccagcacaa cataagcgtg tttctctcca ttggagcagg gcccgtcatt 60
accggataca cgtgcgtttt tctgttcggg attctgggac acttttactt gtattggaaa 120
aaccatcaga gacgacaccg gacaaacagt ttcagtgatg ttttatttcg acatctcatg 180
atcaccgaag aggtctttac cctcaccatt cccgtctggg cgtatcactt aactactcac 240
ggcaacttac cgggctcgtg gtgccgaagt ctcaccttcg ttttttatct aacggtattc 300
gctcgtgcct tcttttacct gctcctcatc tgggaccgat acagcgtaat catctgcaga 360
caccctctcc ccgttaatct gaactacagt caggtcatag gcctgtctgt ctggctggtt 420
gccgtactgt cagcatcacc gttctccatt tttaacggaa gtgtgaaaca atgcctgggc 480
aacatgggca gcatacccag cgaatcgtct gccgttctta acctggaagt gcacctgtgc 540
tccttctggt taccgctcat catgtcggct aactgttact accaagcaaa acgccgagca 600
tcgcctgacc aactccacga actttaccga tgcagtttgc taattaccat tatcacaact 660
tacgctatcg tatggtttcc tttccatctc gctttactca tagacgccct gattagcata 720
agccatgtag aaccctctag cgctctccac tgggcatcca ttgtcgttac ctgtaaatca 780
tttacatttg tatatgcggg cataagccca ctagtgtatt tcacatgctg ccccaccgta 840
cgtcgcgaac tgctgatgtc tctacgtcca ttcttcacct ggatttccag caaaacgcgg 900
cgaggctacg ctccgattaa aacacaacct ttaaacatcc ccgacgagcc gatagataac 960

aagtcaccgc acctgttaaa cgaataa 987

<210> 12
<211> 328
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog rhUS28.4

<400> 12

```
Met Asn Ser Ser Gln His Asn Ile Ser Val Phe Leu Ser Ile Gly Ala
  1               5                  10                  15

Gly Pro Val Ile Thr Gly Tyr Thr Cys Val Phe Leu Phe Gly Ile Leu
             20                  25                  30

Gly His Phe Tyr Leu Tyr Trp Lys Asn His Gln Arg Arg His Arg Thr
         35                  40                  45

Asn Ser Phe Ser Asp Val Leu Phe Arg His Leu Met Ile Thr Glu Glu
     50                  55                  60

Val Phe Thr Leu Thr Ile Pro Val Trp Ala Tyr His Leu Thr Thr His
 65                  70                  75                  80

Gly Asn Leu Pro Gly Ser Trp Cys Arg Ser Leu Thr Phe Val Phe Tyr
                 85                  90                  95

Leu Thr Val Phe Ala Arg Ala Phe Phe Tyr Leu Leu Leu Ile Trp Asp
            100                 105                 110

Arg Tyr Ser Val Ile Ile Cys Arg His Pro Leu Pro Val Asn Leu Asn
        115                 120                 125

Tyr Ser Gln Val Ile Gly Leu Ser Val Trp Leu Val Ala Val Leu Ser
    130                 135                 140

Ala Ser Pro Phe Ser Ile Phe Asn Gly Ser Val Lys Gln Cys Leu Gly
145                 150                 155                 160

Asn Met Gly Ser Ile Pro Ser Glu Ser Ser Ala Val Leu Asn Leu Glu
                165                 170                 175

Val His Leu Cys Ser Phe Trp Leu Pro Leu Ile Met Ser Ala Asn Cys
            180                 185                 190

Tyr Tyr Gln Ala Lys Arg Arg Ala Ser Pro Asp Gln Leu His Glu Leu
        195                 200                 205

Tyr Arg Cys Ser Leu Leu Ile Thr Ile Ile Thr Thr Tyr Ala Ile Val
    210                 215                 220

Trp Phe Pro Phe His Leu Ala Leu Leu Ile Asp Ala Leu Ile Ser Ile
225                 230                 235                 240

Ser His Val Glu Pro Ser Ser Ala Leu His Trp Ala Ser Ile Val Val
                245                 250                 255
```

```
Thr Cys Lys Ser Phe Thr Phe Val Tyr Ala Gly Ile Ser Pro Leu Val
            260                 265                 270

Tyr Phe Thr Cys Cys Pro Thr Val Arg Arg Glu Leu Leu Met Ser Leu
        275                 280                 285

Arg Pro Phe Phe Thr Trp Ile Ser Ser Lys Thr Arg Arg Gly Tyr Ala
    290                 295                 300

Pro Ile Lys Thr Gln Pro Leu Asn Ile Pro Asp Glu Pro Ile Asp Asn
305                 310                 315                 320

Lys Ser Pro His Leu Leu Asn Glu
                325
```

<210> 13
<211> 1452
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.5

<220>
<221> CDS
<222> (1)..(1452)
<223> rhUS28.5

<400> 13

```
atgactacca ccacaatgag tgctaccacg aattccagta ccacgcctca agcaagcagc 60
accacgatga caacgaagac aagcactcct ggcaatacaa ctactggcac tacgtccacc 120
ctgacaacga tatcaacaac ttctaatgct accagcataa cgtctaattt aagcactacc 180
ggaaaccaaa ctgcaactac caatgctact accttcagtt ccacattaac aacatctaca 240
aatataagca gtacattttc gacagtttct accgtcgcat ccaatgcaac atgtaattct 300
acaatcacaa cgaatattac aactgctttt actacagcag caaacactac cgcaagcagc 360
ctcaccagca tcgtaacttc acttgccact accattgaaa ccacatcatt tgattatgat 420
gagtcagcag aagcttgcaa cttaacagac atcgttcata ctactagatc agtgacagtt 480
actttctata ctatcatatt catactcggc cttttgggaa actttctggt tcttatgacc 540
atcatttgga accgtcgcat ttcctttatg gttgaaatat atttcgttaa tctagcaatc 600
tccgatctta tgtttgtatg tactttacca ttttggataa tgtatcttct tgagcacgac 660
gtcatgtcac atgcatcctg tgtagcaatg acagccattt tttattgcgc gctgtttgcc 720
agcactgttt tcctcttgct aattgtttta gacagatgtt acgctattct attaggtaca 780
gaaaaagcaa atagacgttt attgcgcaat gctgtttctg gatgcatgct catgtgggga 840
ttgtgtttca ttttagcatt acctcatttt atctttatga agaaaggaac caacgtatgt 900
gtagcagagt atgaaccagg acttaacaat ttctatgtta tttttatcaa tactgaggtg 960
aacctatgca ccctagtttt gccagccgca gccattatct actggtatct taaactaacc 1020
aaagcactca aaacccatga acgactgcgt cataggctaa cgtctctaaa catagtgtta 1080
gctgttgtca ttgtatttgc tttgttttgg ctgccgtata atctcatgct tatgatgtat 1140
agcttagttc acatgcagat accttgggaa tgcagctctg aaaaaatact gagacgaagt 1200
ttaattatta cagaatccat cgccctcagt cactgttgca tcaaccccat tatctacttg 1260
ctcttcggac ctcgctgtcg aagcgagttc tgtcacctgt tgcgatgttg ctttacgcgc 1320
ttatgtccac acagatcctg gagttccata cgtgcagaga cggtgtccat cagtctcagt 1380
cactcacagg tatctgcatc atctgaggat gatgacaacg atgtgcatga tgaattgcaa 1440
tttttaattt ga                                                    1452
```

<210> 14
<211> 483
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.5

<400> 14
Met Thr Thr Thr Thr Met Ser Ala Thr Thr Asn Ser Ser Thr Thr Pro
1 5 10 15

Gln Ala Ser Ser Thr Thr Met Thr Thr Lys Thr Ser Thr Pro Gly Asn
20 25 30

Thr Thr Thr Gly Thr Thr Ser Thr Leu Thr Thr Ile Ser Thr Thr Ser
35 40 45

Asn Ala Thr Ser Ile Thr Ser Asn Leu Ser Thr Thr Gly Asn Gln Thr
50 55 60

Ala Thr Thr Asn Ala Thr Thr Phe Ser Ser Thr Leu Thr Thr Ser Thr
65 70 75 80

Asn Ile Ser Ser Thr Phe Ser Thr Val Ser Thr Val Ala Ser Asn Ala
85 90 95

Thr Cys Asn Ser Thr Ile Thr Thr Asn Ile Thr Thr Ala Phe Thr Thr
100 105 110

Ala Ala Asn Thr Thr Ala Ser Ser Leu Thr Ser Ile Val Thr Ser Leu
115 120 125

Ala Thr Thr Ile Glu Thr Thr Ser Phe Asp Tyr Asp Glu Ser Ala Glu
130 135 140

Ala Cys Asn Leu Thr Asp Ile Val His Thr Thr Arg Ser Val Thr Val
145 150 155 160

Thr Phe Tyr Thr Ile Ile Phe Ile Leu Gly Leu Leu Gly Asn Phe Leu
165 170 175

Val Leu Met Thr Ile Ile Trp Asn Arg Arg Ile Ser Phe Met Val Glu
180 185 190

Ile Tyr Phe Val Asn Leu Ala Ile Ser Asp Leu Met Phe Val Cys Thr
195 200 205

Leu Pro Phe Trp Ile Met Tyr Leu Leu Glu His Asp Val Met Ser His
210 215 220

Ala Ser Cys Val Ala Met Thr Ala Ile Phe Tyr Cys Ala Leu Phe Ala
225 230 235 240

Ser Thr Val Phe Leu Leu Leu Ile Val Leu Asp Arg Cys Tyr Ala Ile
245 250 255

Leu Leu Gly Thr Glu Lys Ala Asn Arg Arg Leu Leu Arg Asn Ala Val
260 265 270

Ser Gly Cys Met Leu Met Trp Gly Leu Cys Phe Ile Leu Ala Leu Pro
275 280 285

His Phe Ile Phe Met Lys Lys Gly Thr Asn Val Cys Val Ala Glu Tyr
290 295 300

Glu Pro Gly Leu Asn Asn Phe Tyr Val Ile Phe Ile Asn Thr Glu Val
305 310 315 320

Asn Leu Cys Thr Leu Val Leu Pro Ala Ala Ala Ile Ile Tyr Trp Tyr
325 330 335

Leu Lys Leu Thr Lys Ala Leu Lys Thr His Glu Arg Leu Arg His Arg
340 345 350

Leu Thr Ser Leu Asn Ile Val Leu Ala Val Val Ile Val Phe Ala Leu
355 360 365

Phe Trp Leu Pro Tyr Asn Leu Met Leu Met Met Tyr Ser Leu Val His
370 375 380

Met Gln Ile Pro Trp Glu Cys Ser Ser Glu Lys Ile Leu Arg Arg Ser
385 390 395 400

Leu Ile Ile Thr Glu Ser Ile Ala Leu Ser His Cys Cys Ile Asn Pro
405 410 415

Ile Ile Tyr Leu Leu Phe Gly Pro Arg Cys Arg Ser Glu Phe Cys His
420 425 430

Leu Leu Arg Cys Cys Phe Thr Arg Leu Cys Pro His Arg Ser Trp Ser
435 440 445

Ser Ile Arg Ala Glu Thr Val Ser Ile Ser Leu Ser His Ser Gln Val
450 455 460

Ser Ala Ser Ser Glu Asp Asp Asp Asn Asp Val His Asp Glu Leu Gln
465 470 475 480

Phe Leu Ile

<210> 15
<211> 1296
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL78

<220>
<221> CDS
<222> (1)..(1296)
<223> HCMV AD169 UL78

<400> 15
atgtcccctt ctgtggagga gactacctca gtcaccgagt ccatcatgtt cgctattgtg 60
agtttcaaac acatgggccc gttcgaaggc tactctatgt cggccgatcg cgccgcctcg 120
gatctactca tcggcatgtt cggctccgtt agcctggtca acctgctgac tatcatcggt 180
tgcctctggg tgttgcgtgt tacgcggccg cccgtgtccg tgatgatttt tacttggaat 240

```
ctggtactta gtcagttttt ttccatcctg gccaccatgt tgtccaaggg tatcatgctg 300
cgtggcgctc taaatctcag cctctgtcgc ttagtgctct ttgtcgacga cgtgggccta 360
tattcgacgg cgttgttttt cctctttctg atactggatc gtctgtcggc catatcttac 420
ggccgtgatc tctggcatca tgagacgcgc gaaaacgccg gcgtggcgct ctacgcggtc 480
gcctttgcct gggttctttc catcgtagcc gctgtgccca ccgccgctac gggttcactg 540
gactaccgtt ggctaggctg tcagatccct atacagtatg ccgcggtgga cctcaccatc 600
aagatgtggt ttttgctggg ggcgcccatg atcgccgtac tggctaacgt ggtagagttg 660
gcctacagcg atcggcgcga ccacgtctgg tcctacgtgg gtcgtgtctg caccttctac 720
gtgacgtgtc tcatgctgtt tgtgccctac tactgcttca gagtcctacg cggtgtactg 780
cagcccgcta gcgcggccgg caccggtttc ggcattatgg attacgtgga attggctacg 840
cgtacccttc tcaccatgcg tcttggcatt ctgccgctct ttatcattgc gttcttctcc 900
cgcgagccca ccaaggatct ggatgactcc tttgattatc tggtcgagag atgtcagcaa 960
agctgccacg gtcatttcgt acgtcggttg gtgcaggcgt tgaagcgggc tatgtatagc 1020
gtggagctgg ccgtgtgtta cttttctacg tccgtccgag acgtcgccga ggcggtgaaa 1080
aagtcctcca gccgttgtta cgccgacgcg acgtcggcgg ccgttgtggt aacgacaacc 1140
acgtcggaga aagccacgtt ggtggagcac gcggaaggca tggcttccga aatgtgtcct 1200
gggactacga tcgatgtttc ggccgaaagt tcctccgtcc tctgcaccga cggcgaaaac 1260
accgtcgcgt cggacgcgac ggtgacggca ttatga                          1296
```

<210> 16
<211> 431
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open reading frame UL78

<400> 16

```
Met Ser Pro Ser Val Glu Glu Thr Thr Ser Val Thr Glu Ser Ile Met
  1               5                  10                  15

Phe Ala Ile Val Ser Phe Lys His Met Gly Pro Phe Glu Gly Tyr Ser
             20                  25                  30

Met Ser Ala Asp Arg Ala Ala Ser Asp Leu Leu Ile Gly Met Phe Gly
         35                  40                  45

Ser Val Ser Leu Val Asn Leu Leu Thr Ile Ile Gly Cys Leu Trp Val
     50                  55                  60

Leu Arg Val Thr Arg Pro Pro Val Ser Val Met Ile Phe Thr Trp Asn
 65                  70                  75                  80

Leu Val Leu Ser Gln Phe Phe Ser Ile Leu Ala Thr Met Leu Ser Lys
                 85                  90                  95

Gly Ile Met Leu Arg Gly Ala Leu Asn Leu Ser Leu Cys Arg Leu Val
            100                 105                 110

Leu Phe Val Asp Asp Val Gly Leu Tyr Ser Thr Ala Leu Phe Phe Leu
        115                 120                 125

Phe Leu Ile Leu Asp Arg Leu Ser Ala Ile Ser Tyr Gly Arg Asp Leu
    130                 135                 140

Trp His His Glu Thr Arg Glu Asn Ala Gly Val Ala Leu Tyr Ala Val
145                 150                 155                 160
```

```
Ala Phe Ala Trp Val Leu Ser Ile Val Ala Ala Val Pro Thr Ala Ala
                165                 170                 175

Thr Gly Ser Leu Asp Tyr Arg Trp Leu Gly Cys Gln Ile Pro Ile Gln
            180                 185                 190

Tyr Ala Ala Val Asp Leu Thr Ile Lys Met Trp Phe Leu Leu Gly Ala
        195                 200                 205

Pro Met Ile Ala Val Leu Ala Asn Val Val Glu Leu Ala Tyr Ser Asp
    210                 215                 220

Arg Arg Asp His Val Trp Ser Tyr Val Gly Arg Val Cys Thr Phe Tyr
225                 230                 235                 240

Val Thr Cys Leu Met Leu Phe Val Pro Tyr Tyr Cys Phe Arg Val Leu
                245                 250                 255

Arg Gly Val Leu Gln Pro Ala Ser Ala Ala Gly Thr Gly Phe Gly Ile
            260                 265                 270

Met Asp Tyr Val Glu Leu Ala Thr Arg Thr Leu Leu Thr Met Arg Leu
        275                 280                 285

Gly Ile Leu Pro Leu Phe Ile Ile Ala Phe Phe Ser Arg Glu Pro Thr
    290                 295                 300

Lys Asp Leu Asp Asp Ser Phe Asp Tyr Leu Val Glu Arg Cys Gln Gln
305                 310                 315                 320

Ser Cys His Gly His Phe Val Arg Arg Leu Val Gln Ala Leu Lys Arg
                325                 330                 335

Ala Met Tyr Ser Val Glu Leu Ala Val Cys Tyr Phe Ser Thr Ser Val
            340                 345                 350

Arg Asp Val Ala Glu Ala Val Lys Lys Ser Ser Ser Arg Cys Tyr Ala
        355                 360                 365

Asp Ala Thr Ser Ala Ala Val Val Val Thr Thr Thr Thr Ser Glu Lys
    370                 375                 380

Ala Thr Leu Val Glu His Ala Glu Gly Met Ala Ser Glu Met Cys Pro
385                 390                 395                 400

Gly Thr Thr Ile Asp Val Ser Ala Glu Ser Ser Ser Val Leu Cys Thr
                405                 410                 415

Asp Gly Glu Asn Thr Val Ala Ser Asp Ala Thr Val Thr Ala Leu
            420                 425                 430
```

<210> 17
<211> 1140
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog (rhUL78)

<220>
<221> CDS
<222> (1)..(1140)
<223> rhUL78

<400> 17
atgattacgg agcgcgtcct cgcaggcatc ctcgcgggca tgacggccgc ggggagtttg 60
gtcattctcc tcgcggttgt tatgtggttg aacatgttag atcgcgctgg catgccaatg 120
gccgttgggc attacacagg gaacctggtg ttgactcagg tcatctgtat cttctccatg 180
ctggcgtcta aaattgttgg catgacgagt gcggccaaca tgggcttctg cggcatcgtg 240
gtttttctgg aagacactgg cctctatgtc acctcgctgc tcttcatgtt tatgatcctg 300
gatcgcatgg cggcttttct taacgggcgt cttttctgga ggcagcagac gacgaagcag 360
aatctgagta caagcgtgta cattattctg ttttgctggg tgttgggaat ggccgcggct 420
gttcccagcg cggctgtggc tgcacccaat tccaggtggg aacgctgcga aattccagtg 480
tcatatgccg caatcgacat gattgtgaag ctctggtttg tgctgttggc acccgtcgtg 540
ctgattatgg ctgtgatcat tcaatcttcc tatcatcgtg atcgggagag gatctggtac 600
tatgccagac gtgtgttcat gttctacacg gcctgctttg tcatgatggt gccttattac 660
ttcgtcagag tcatgctgag cgactttgct ttggttgata taaaaacaaa aacggcgaac 720
agcgacggtt gtgattcgac atttcttgat tatctgaaca tgttcactca cgtgatttac 780
agttttaagt tggtggtgtt tgctttgttc attgtcctgt tttgctccat aaacccgatg 840
gaaacgctgg aagaatgctt ggagagggcc gatgctgaga ggcaaagtcg gtcagaagca 900
tcccagggtg aaaggaggct gccaatcaac acatgctgta taaagttgat tgaattgata 960
aagcagtatg taagcactct ctctaaagcc acgagggaca attctggcga aagggccaat 1020
ttgccagaga atgctgaaga tattggaaca actggcagtg atcagctacc gactgaggtc 1080
accgtgaccc caaattcatc ggctgtgttt agcactggag gaacggtgtc tccagtctaa 1140

<210> 18
<211> 379
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog
(rhUL78)

<400> 18
Met Ile Thr Glu Arg Val Leu Ala Gly Ile Leu Ala Gly Met Thr Ala
1 5 10 15

Ala Gly Ser Leu Val Ile Leu Leu Ala Val Val Met Trp Leu Asn Met
20 25 30

Leu Asp Arg Ala Gly Met Pro Met Ala Val Gly His Tyr Thr Gly Asn
35 40 45

Leu Val Leu Thr Gln Val Ile Cys Ile Phe Ser Met Leu Ala Ser Lys
50 55 60

Ile Val Gly Met Thr Ser Ala Ala Asn Met Gly Phe Cys Gly Ile Val
65 70 75 80

Val Phe Leu Glu Asp Thr Gly Leu Tyr Val Thr Ser Leu Leu Phe Met
85 90 95

Phe Met Ile Leu Asp Arg Met Ala Ala Phe Leu Asn Gly Arg Leu Phe
100 105 110

Trp Arg Gln Gln Thr Thr Lys Gln Asn Leu Ser Thr Ser Val Tyr Ile
115 120 125

```
Ile Leu Phe Cys Trp Val Leu Gly Met Ala Ala Ala Val Pro Ser Ala
    130                 135                 140

Ala Val Ala Ala Pro Asn Ser Arg Trp Glu Arg Cys Glu Ile Pro Val
145                 150                 155                 160

Ser Tyr Ala Ala Ile Asp Met Ile Val Lys Leu Trp Phe Val Leu Leu
                165                 170                 175

Ala Pro Val Val Leu Ile Met Ala Val Ile Ile Gln Ser Ser Tyr His
            180                 185                 190

Arg Asp Arg Glu Arg Ile Trp Tyr Tyr Ala Arg Arg Val Phe Met Phe
        195                 200                 205

Tyr Thr Ala Cys Phe Val Met Met Val Pro Tyr Tyr Phe Val Arg Val
    210                 215                 220

Met Leu Ser Asp Phe Ala Leu Val Asp Ile Lys Thr Lys Thr Ala Asn
225                 230                 235                 240

Ser Asp Gly Cys Asp Ser Thr Phe Leu Asp Tyr Leu Asn Met Phe Thr
                245                 250                 255

His Val Ile Tyr Ser Phe Lys Leu Val Val Phe Ala Leu Phe Ile Val
            260                 265                 270

Leu Phe Cys Ser Ile Asn Pro Met Glu Thr Leu Glu Glu Cys Leu Glu
        275                 280                 285

Arg Ala Asp Ala Glu Arg Gln Ser Arg Ser Glu Ala Ser Gln Gly Glu
    290                 295                 300

Arg Arg Leu Pro Ile Asn Thr Cys Cys Ile Lys Leu Ile Glu Leu Ile
305                 310                 315                 320

Lys Gln Tyr Val Ser Thr Leu Ser Lys Ala Thr Arg Asp Asn Ser Gly
                325                 330                 335

Glu Arg Ala Asn Leu Pro Glu Asn Ala Glu Asp Ile Gly Thr Thr Gly
            340                 345                 350

Ser Asp Gln Leu Pro Thr Glu Val Thr Val Thr Pro Asn Ser Ser Ala
        355                 360                 365

Val Phe Ser Thr Gly Gly Thr Val Ser Pro Val
    370                 375
```

<210> 19
<211> 1173
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open reading frame UL33

<220>
<221> CDS
<222> (1)..(1173)
<223> HCMV AD169 UL33

<400> 19
atgacagggc cgctattcgc cattcgaacc accgaagccg tactcaacac attcatcatc 60
ttcgtgggcg gtccacttaa cgccatagtg ttgatcacgc agctgctcac gaatcgcgtg 120
cttggctatt cgacgcccac catttacatg accaacctct actctactaa ttttctcacg 180
cttactgtgc tacccttttat cgtactcagc aaccagtggc tgttgccggc cggcgtggcc 240
tcgtgtaaat ttctatcggt gatctactac tcaagctgca cagtgggctt tgccaccgta 300
gctctgatcg ccgccgatcg ttatcgcgtc cttcataaac gaacatacgc acgccaatca 360
taccgttcaa cctatatgat tttgctattg acatggctcg ctggactaat tttttccgtg 420
cccgcagctg tttacaccac ggtggtgatg catcacgatg ccaacgatac caataatact 480
aatgggcacg ccacctgtgt actgtacttc gtagctgaag aagtgcacac agtgctgctt 540
tcgtggaaag tgctgctgac gatggtatgg ggtgccgcac ccgtgataat gatgacgtgg 600
ttctacgcat tcttctactc aaccgtacag cgcacgtcac agaaacaaag gagtcgtacc 660
ttaacctttg ttagcgtgct actcatctcc ttcgtggcgc tacaaactcc ctacgtctct 720
ctcatgatct tcaacagtta tgccacaacc gcctggccca tgcagtgtga acacctcaca 780
ctgcgacgca ccattggcac gctggcgcgt gtggtgcccc acctacactg cctcattaat 840
cccatcctgt acgcgctgct gggtcatgat tttctgcaac gcatgcggca gtgtttccgc 900
ggtcagttgc tggaccgccg cgctttcctg agatcgcagc agaatcagcg agctacagcg 960
gagacaaatc tagcggctgg caacaattca caatcagtgg ctacgtcatt agacaccaat 1020
agcaaaaact acaatcagca cgccaaacgc agcgtgtctt tcaattttcc cagcggtacg 1080
tggaaaggcg gccagaaaac cgcgtccaac gacacatcca caaaaatccc ccatcgactc 1140
tcacaatcgc atcataacct cagcggggta tga 1173

<210> 20
<211> 390
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL33

<400> 20
Met Thr Gly Pro Leu Phe Ala Ile Arg Thr Thr Glu Ala Val Leu Asn
1 5 10 15

Thr Phe Ile Ile Phe Val Gly Gly Pro Leu Asn Ala Ile Val Leu Ile
20 25 30

Thr Gln Leu Leu Thr Asn Arg Val Leu Gly Tyr Ser Thr Pro Thr Ile
35 40 45

Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe Leu Thr Leu Thr Val Leu
50 55 60

Pro Phe Ile Val Leu Ser Asn Gln Trp Leu Leu Pro Ala Gly Val Ala
65 70 75 80

Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr Ser Ser Cys Thr Val Gly
85 90 95

Phe Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Leu His
100 105 110

Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg Ser Thr Tyr Met Ile Leu
115 120 125

```
Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe Ser Val Pro Ala Ala Val
    130                 135                 140

Tyr Thr Thr Val Val Met His His Asp Ala Asn Asp Thr Asn Asn Thr
145                 150                 155                 160

Asn Gly His Ala Thr Cys Val Leu Tyr Phe Val Ala Glu Glu Val His
                165                 170                 175

Thr Val Leu Leu Ser Trp Lys Val Leu Leu Thr Met Val Trp Gly Ala
            180                 185                 190

Ala Pro Val Ile Met Met Thr Trp Phe Tyr Ala Phe Phe Tyr Ser Thr
        195                 200                 205

Val Gln Arg Thr Ser Gln Lys Gln Arg Ser Arg Thr Leu Thr Phe Val
    210                 215                 220

Ser Val Leu Leu Ile Ser Phe Val Ala Leu Gln Thr Pro Tyr Val Ser
225                 230                 235                 240

Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr Ala Trp Pro Met Gln Cys
                245                 250                 255

Glu His Leu Thr Leu Arg Arg Thr Ile Gly Thr Leu Ala Arg Val Val
            260                 265                 270

Pro His Leu His Cys Leu Ile Asn Pro Ile Leu Tyr Ala Leu Leu Gly
        275                 280                 285

His Asp Phe Leu Gln Arg Met Arg Gln Cys Phe Arg Gly Gln Leu Leu
    290                 295                 300

Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln Asn Gln Arg Ala Thr Ala
305                 310                 315                 320

Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser Gln Ser Val Ala Thr Ser
                325                 330                 335

Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln His Ala Lys Arg Ser Val
            340                 345                 350

Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys Gly Gly Gln Lys Thr Ala
        355                 360                 365

Ser Asn Asp Thr Ser Thr Lys Ile Pro His Arg Leu Ser Gln Ser His
    370                 375                 380

His Asn Leu Ser Gly Val
385                 390
```

<210> 21
<211> 1239
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open reading frame UL33 splice variant (UL33 spliced)

<220>
<221> CDS
<222> (1)..(1239)
<223> HCMV AD169 UL33 spliced

<400> 21
atggacacca tcatccacaa ctcgacccgc aacaacactc ctccgcacat caatgacact 60
tgcaacatga cagggccgct attcgccatt cgaaccaccg aagccgtact caacacattc 120
atcatcttcg tgggcggtcc acttaacgcc atagtgttga tcacgcagct gctcacgaat 180
cgcgtgcttg gctattcgac gcccaccatt tacatgacca acctctactc tactaatttt 240
ctcacgctta ctgtgctacc ctttatcgta ctcagcaacc agtggctgtt gccggccggc 300
gtggcctcgt gtaaatttct atcggtgatc tactactcaa gctgcacagt gggctttgcc 360
accgtagctc tgatcgccgc cgatcgttat cgcgtccttc ataaacgaac atacgcacgc 420
caatcatacc gttcaaccta tatgattttg ctattgacat ggctcgctgg actaattttt 480
tccgtgcccg cagctgttta caccacggtg gtgatgcatc acgatgccaa cgataccaat 540
aatactaatg ggcacgccac ctgtgtactg tacttcgtag ctgaagaagt gcacacagtg 600
ctgctttcgt ggaaagtgct gctgacgatg gtatggggtg ccgcacccgt gataatgatg 660
acgtggttct acgcattctt ctactcaacc gtacagcgca cgtcacagaa acaaaggagt 720
cgtaccttaa cctttgttag cgtgctactc atctccttcg tggcgctaca aactccctac 780
gtctctctca tgatcttcaa cagttatgcc acaaccgcct ggcccatgca gtgtgaacac 840
ctcacactgc gacgcaccat tggcacgctg gcgcgtgtgg tgccccacct acactgcctc 900
attaatccca tcctgtacgc gctgctgggt catgattttc tgcaacgcat gcggcagtgt 960
ttccgcggtc agttgctgga ccgccgcgct ttcctgagat cgcagcagaa tcagcgagct 1020
acagcggaga caaatctagc ggctggcaac aattcacaat cagtggctac gtcattagac 1080
accaatagca aaaactacaa tcagcacgcc aaacgcagcg tgtctttcaa ttttcccagc 1140
ggtacgtgga aaggcggcca gaaaaccgcg tccaacgaca catccacaaa aatcccccat 1200
cgactctcac aatcgcatca taacctcagc ggggtatga 1239

<210> 22
<211> 412
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL33 splice variant (UL33 spliced)

<400> 22
Met Asp Thr Ile Ile His Asn Ser Thr Arg Asn Asn Thr Pro Pro His
1 5 10 15

Ile Asn Asp Thr Cys Asn Met Thr Gly Pro Leu Phe Ala Ile Arg Thr
20 25 30

Thr Glu Ala Val Leu Asn Thr Phe Ile Ile Phe Val Gly Gly Pro Leu
35 40 45

Asn Ala Ile Val Leu Ile Thr Gln Leu Leu Thr Asn Arg Val Leu Gly
50 55 60

Tyr Ser Thr Pro Thr Ile Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe
65 70 75 80

Leu Thr Leu Thr Val Leu Pro Phe Ile Val Leu Ser Asn Gln Trp Leu
85 90 95

Leu Pro Ala Gly Val Ala Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr
100 105 110

Ser Ser Cys Thr Val Gly Phe Ala Thr Val Ala Leu Ile Ala Ala Asp
115 120 125

Arg Tyr Arg Val Leu His Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg
130 135 140

Ser Thr Tyr Met Ile Leu Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe
145 150 155 160

Ser Val Pro Ala Ala Val Tyr Thr Thr Val Val Met His His Asp Ala
165 170 175

Asn Asp Thr Asn Asn Thr Asn Gly His Ala Thr Cys Val Leu Tyr Phe
180 185 190

Val Ala Glu Glu Val His Thr Val Leu Leu Ser Trp Lys Val Leu Leu
195 200 205

Thr Met Val Trp Gly Ala Ala Pro Val Ile Met Met Thr Trp Phe Tyr
210 215 220

Ala Phe Phe Tyr Ser Thr Val Gln Arg Thr Ser Gln Lys Gln Arg Ser
225 230 235 240

Arg Thr Leu Thr Phe Val Ser Val Leu Leu Ile Ser Phe Val Ala Leu
245 250 255

Gln Thr Pro Tyr Val Ser Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr
260 265 270

Ala Trp Pro Met Gln Cys Glu His Leu Thr Leu Arg Arg Thr Ile Gly
275 280 285

Thr Leu Ala Arg Val Val Pro His Leu His Cys Leu Ile Asn Pro Ile
290 295 300

Leu Tyr Ala Leu Leu Gly His Asp Phe Leu Gln Arg Met Arg Gln Cys
305 310 315 320

Phe Arg Gly Gln Leu Leu Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln
325 330 335

Asn Gln Arg Ala Thr Ala Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser
340 345 350

Gln Ser Val Ala Thr Ser Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln
355 360 365

His Ala Lys Arg Ser Val Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys
370 375 380

Gly Gly Gln Lys Thr Ala Ser Asn Asp Thr Ser Thr Lys Ile Pro His
385 390 395 400

Arg Leu Ser Gln Ser His His Asn Leu Ser Gly Val
405 410

<210> 23
<211> 990
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
(rhUL33)

<220>
<221> CDS
<222> (1)..(990)
<223> rhUL33

<400> 23
atgaccaatc tttactctgc caattttctc accttgatag tacttccttt tatcgtttta 60
agcaatcaac acctttacc tgccagtgca gtaacctgta aatttctctc cctgttgtac 120
tactctagct gcagcgtagg ttttgctaca gtggcactga tagcggccga ccgataccga 180
gtgattcatc gccgaactca agctcgccaa tcctaccgta acacatatat gatagtaggc 240
ttaacgtggc tcattggctt gatctgcgct acccccgggg gggtctacac aaccattgta 300
gctcaccgcg atggggaaag tgatgctcaa agacacaata cttgcattat gcactttgcg 360
tatgatgaag tttacgtcct catggtctgg aaacttctca tcgttttagt ctggggcata 420
gtgccagttg tcatgatgag ctggttttac gcgtttttt acaatactgt acaaagaaca 480
gccaaaaaac aacaacgtac gttgaaattc gtaaaggtat tactcctgtc attcatcatc 540
atccaaactc cctatgtgtc aatcatgatt tttaacacgt atgccaccgt aggatggccg 600
atggaatgcg ccgatctaac tagacgccga gtcatcaaca cgttttcccg tctcgtcccc 660
aatctacatt gcatggtcaa ccccatcctc tacgctctca tgggaaatga ctttgtgtct 720
aaagtgggcc aatgctttcg gggggaactc acgaaccgtc gaacttttct gcgttccaag 780
caacaagccc gcaactcgga cgatgtaccg acaattgtca gtcaacaacc cgccacaccc 840
accatcgtca ataagcccga aaaaaacccg cacgtaaaac gcggtgtatc tttcagcgtc 900
agcgcatctt ccgaactcgc agcggccaaa aaagccaaag acaaagccaa gcggctttcc 960
atgtcccacc aaaacctacg tctgacgtga 990

<210> 24
<211> 329
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
(rhUL33)

<400> 24
Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
1 5 10 15

Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
20 25 30

Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
35 40 45

Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
50 55 60

Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
65 70 75 80

Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
85 90 95

```
Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
            100                 105                 110

Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
        115                 120                 125

Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
    130                 135                 140

Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
145                 150                 155                 160

Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu Leu
                165                 170                 175

Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
            180                 185                 190

Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
        195                 200                 205

Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
    210                 215                 220

Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
225                 230                 235                 240

Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
                245                 250                 255

Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
            260                 265                 270

Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
        275                 280                 285

Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
    290                 295                 300

Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
305                 310                 315                 320

Met Ser His Gln Asn Leu Arg Leu Thr
                325
```

<210> 25
<211> 1328
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice variant homolog (rhUL33 spliced)

<220>
<221> CDS
<222> (1)..(1328)
<223> rhUL33 spliced

<400> 25
atggcagtca ctttacgagg cggcagcccg ataaacttta aactcatgat tgtcagccac 60
agaaaccgga aatttcacga gatacggctg tttcagcgtt ctgctatccg tccaggcggg 120
ttatggaaac cattcttcac aaccgaacga gtgaaactaa ttccattttg cacatcaaca 180
ccacctgcaa tgtgaccgac tcactgtacg ccgccaaact aggcgaagcc ctcgtgaaca 240
gcgcgctagc tttattcggt acccccctca acgccatcgt cctcgtcaca cagctattgg 300
ccaaccgagt tcatggatac tccaccccga ttatctacat gaccaatctt tactctgcca 360
attttctcac cttgatagta cttcctttta tcgttttaag caatcaacac cttttacctg 420
ccagtgcagt aacctgtaaa tttctctccc tgttgtacta ctctagctgc agcgtaggtt 480
ttgctacagt ggcactgata gcggccgacc gataccgagt gattcatcgc cgaactcaag 540
ctcgccaatc ctaccgtaac acatatatga tagtaggctt aacgtggctc attggcttga 600
tctgcgctac ccccgggggg gtctacacaa ccattgtagc tcaccgcgat ggggaaagtg 660
atgctcaaag acacaatact tgcattatgc actttgcgta tgatgaagtt tacgtcctca 720
tggtctggaa acttctcatc gttttagtct ggggcatagt gccagttgtc atgatgagct 780
ggttttacgc gtttttttac aatactgtac aaagaacagc caaaaaacaa caacgtacgt 840
tgaaattcgt aaaggtatta ctcctgtcat tcatcatcat ccaaactccc tatgtgtcaa 900
tcatgatttt taacacgtat gccaccgtag gatggccgat ggaatgcgcc gatctaacta 960
gacgccgagt catcaacacg ttttcccgtc tcgtccccaa tctacattgc atggtcaacc 1020
ccatcctcta cgctctcatg ggaaatgact ttgtgtctaa agtgggccaa tgctttcggg 1080
gggaactcac gaaccgtcga acttttctgc gttccaagca acaagcccgc aactcggacg 1140
atgtaccgac aattgtcagt caacaacccg ccacacccac catcgtcaat aagcccgaaa 1200
aaaacccgca cgtaaaacgc ggtgtatctt tcagcgtcag cgcatcttcc gaactcgcag 1260
cggccaaaaa agccaaagac aaagccaagc ggctttccat gtcccaccaa aacctacgtc 1320
tgacgtga 1328

<210> 26
<211> 441
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
variant homolog (rhUL33 spliced)

<400> 26
Met Ala Val Thr Leu Arg Gly Gly Ser Pro Ile Asn Phe Lys Leu Met
1 5 10 15

Ile Val Ser His Arg Asn Arg Lys Phe His Glu Ile Arg Leu Phe Gln
20 25 30

Arg Ser Ala Ile Arg Pro Gly Gly Leu Trp Lys Pro Phe Phe Thr Thr
35 40 45

Glu Arg Glu Thr Asn Ser Ile Leu His Ile Asn Thr Thr Cys Asn Val
50 55 60

Thr Asp Ser Leu Tyr Ala Ala Lys Leu Gly Glu Ala Leu Val Asn Ser
65 70 75 80

Ala Leu Ala Leu Phe Gly Thr Pro Leu Asn Ala Ile Val Leu Val Thr
85 90 95

Gln Leu Leu Ala Asn Arg Val His Gly Tyr Ser Thr Pro Ile Ile Tyr
100 105 110

Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
115 120 125

Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
130 135 140

Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
145 150 155 160

Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
165 170 175

Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
180 185 190

Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
195 200 205

Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
210 215 220

Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
225 230 235 240

Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
245 250 255

Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
260 265 270

Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu Leu
275 280 285

Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
290 295 300

Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
305 310 315 320

Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
325 330 335

Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
340 345 350

Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
355 360 365

Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
370 375 380

Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
385 390 395 400

Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
405 410 415

Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
420 425 430

Met Ser His Gln Asn Leu Arg Leu Thr
435 440

<210> 27
<211> 2100
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice variant homolog (rhUL33 spliced) nucleotide sequence segment that extends 1000 nucleotides upstream and downstream of the rhUL33 reading frame

<220>
<221> exon
<222> (603)..(752)
<223> exon 1

<220>
<221> intron
<222> (753)..(830)

<220>
<221> exon
<222> (831)..(2006)
<223> exon 2

<220>
<221> misc_feature
<222> (1017)..(2006)
<223> unspliced gene

<400> 27
cggccaagat gtcccaagag gttctgacat gaacaatcac ttttccgaga tagatgagtt 60
tgttagtggc atttaccaga gaactattgg agtgacgctc aagatgaagc ttcactggcc 120
gtatttcgaa catattgtta gatatagcta gtaaagaatc ttctaaagcc atgacgtctt 180
tctgacgaag ttgaataaat tctatctcac cagtacccaa aggctgacac tcagacaact 240
ttgccaaggc cgttgcaccc accatggcat tctgaatcac agtaacatcc gtccgagaat 300
cgtcaccaaa aacggtggcc tccaaagttc gcaggtgagg ccgagccttt actggatctc 360
ggaagggata catgtgtgct cgccgagtga cagcattagc attaacctca aactcatcta 420
aaagcgatga taaatcagga atatgatagc gcaattctcg atagtaggcc aaccagagga 480
ctaattggtt gaacagacag ctccgtctgt gcaaaaactt ttcgccgcat tttctgagaa 540
ttttaggatg ctgctctaaa tctacgttct ctttagtcgg cagggtcttt aaaaagttag 600
tgatggcagt cactttacga ggcggcagcc cgataaactt taaactcatg attgtcagcc 660
acagaaaccg gaaatttcac gagatacggc tgtttcagcg ttctgctatc cgtccaggcg 720
ggttatggaa accattcttc acaaccgaac ggtgagtgac atttaagaca gtttaatagc 780
caacactcgt aacgtctcgg aagctgataa gtttcgtttt tccacagagt gaaactaatt 840
ccattttgca catcaacacc acctgcaatg tgaccgactc actgtacgcc gccaaactag 900
gcgaagccct cgtgaacagc gcgctagctt tattcggtac ccccctcaac gccatcgtcc 960
tcgtcacaca gctattggcc aaccgagttc atggatactc caccccgatt atctacatga 1020
ccaatcttta ctctgccaat tttctcacct tgatagtact tccttttatc gttttaagca 1080
atcaacacct tttacctgcc agtgcagtaa cctgtaaatt tctctccctg ttgtactact 1140
ctagctgcag cgtaggtttt gctacagtgg cactgatagc ggccgaccga taccgagtga 1200
ttcatcgccg aactcaagct cgccaatcct accgtaacac atatatgata gtaggcttaa 1260
cgtggctcat tggcttgatc tgcgctaccc ccgggggggt ctacacaacc attgtagctc 1320
accgcgatgg ggaaagtgat gctcaaagac acaatacttg cattatgcac tttgcgtatg 1380
atgaagttta cgtcctcatg gtctggaaac ttctcatcgt tttagtctgg ggcatagtgc 1440
cagttgtcat gatgagctgg ttttacgcgt ttttttacaa tactgtacaa agaacagcca 1500
aaaaacaaca acgtacgttg aaattcgtaa aggtattact cctgtcattc atcatcatcc 1560
aaactcccta tgtgtcaatc atgattttta acacgtatgc caccgtagga tggccgatgg 1620
aatgcgccga tctaactaga cgccgagtca tcaacacgtt ttcccgtctc gtccccaatc 1680
tacattgcat ggtcaacccc atcctctacg ctctcatggg aaatgacttt gtgtctaaag 1740

tgggccaatg ctttcggggg gaactcacga accgtcgaac ttttctgcgt tccaagcaac 1800
aagcccgcaa ctcggacgat gtaccgacaa ttgtcagtca acaacccgcc acacccacca 1860
tcgtcaataa gcccgaaaaa aacccgcacg taaaacgcgg tgtatctttc agcgtcagcg 1920
catcttccga actcgcagcg gccaaaaaag ccaaagacaa agccaagcgg ctttccatgt 1980
cccaccaaaa cctacgtctg acgtgaattt tcctagaggc tgcctccacg ggtttacata 2040
catatctcgg tacttgctac acttgatcac tttactgcgg acaccacggc caatcgcatc 2100

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.1 amplification primer sequence (upper strand)

<400> 28
tatgaataac acatcttgca acttc 25

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.1 amplification primer sequence (lower strand)

<400> 29
cacacagacc acatgtac 18

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.2 amplification primer sequence (upper strand)

<400> 30
attcaacatg accaacgccg g 21

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.2 amplification primer sequence (lower strand)

<400> 31
gcatttccgt ggattcg 17

<210> 32
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.3 amplification primer sequence (upper strand)

<400> 32
catgaccaac actaac 16

<210> 33
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.3 amplification primer sequence (lower strand)

<400> 33
gagtcttttg tgagcc 16

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.4 amplification primer sequence (upper strand)

<400> 34
tatgaattcg agccagcac 19

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.4 amplification primer sequence (lower strand)

<400> 35
gtacgcgact aagacagag 19

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.5 amplification primer sequence (upper strand)

<400> 36
aaagatgact accaccac 18

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUS28.5 amplification primer sequence (lower strand)

<400> 37
ataacctagc acctcccc 18

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL78 amplification primer sequence (upper strand)

<400> 38
ctgaaaccat gattacgg 18

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL78 amplification primer sequence (lower strand)

<400> 39
cacgcagcac aagagcac 18

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL33 amplification primer sequence (upper strand)

<400> 40
catgaccaat ctttactc 18

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL33 amplification primer sequence (lower strand)

<400> 41
gtgtcgccac tcctaccc 18

<210> 42
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL33 splice amplification primer sequence (upper strand)

<400> 42
aagttagtga tggcagtc 18

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog rhUL33 splice amplification primer sequence (lower strand)

<400> 43
gtatgtaaac ccgtggag 18

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV specific primer able to amplify the rhCMV immediate early 2 gene

<400> 44
gccaatgcat cctctggatg tattgtga 28

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV specific primer able to amplify the rhCMV immediate early 2 gene

<400> 45
tgcttgggga atctctgcac 20

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV specific primer able to amplify the rhCMV immediate early 2 gene

<400> 46
cccttcctga ctactaatgt ac 22

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV specific primer able to amplify the rhCMV immediate early 2 gene

<400> 47
ttggggaatc tctgcacaag 20

<210> 48
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open reading frame US28

<400> 48
Met Thr Pro Thr Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15

Asp Glu Asp Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
20 25 30

```
Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
          35                  40                  45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
      50                  55                  60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
 65                  70                  75                  80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
                 85                  90                  95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
            100                 105                 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
        115                 120                 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
    130                 135                 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
145                 150                 155                 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
                165                 170                 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
            180                 185                 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
        195                 200                 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
    210                 215                 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
225                 230                 235                 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
                245                 250                 255

Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
            260                 265                 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
        275                 280                 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
    290                 295                 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
305                 310                 315                 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
                325                 330                 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
            340                 345                 350

Ile Pro
```